

Biochemistry. In the article "Expression cloning of a cDNA for human ceramide glucosyltransferase that catalyzes the first glycosylation step of glycosphingolipid synthesis" by S. Ichikawa, H. Sakiyama, G. Suzuki, K. I.-P. J. Hidari, and Y. Hirabayashi, which appeared in number 10, May 14, of *Proc.*

Natl. Acad. Sci. USA (93, 4638–4643), the authors request that the following error be noted. In the sequence shown in Fig 6A on p. 4642 two "G"s were inadvertently dropped in the series of four "G"s between positions –270 and –273. The correct sequence is given below.¹

A

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-290                                     (5') GAGGCGAACCCGAGCGCGG -271
-270 GCGCGGTCGCCCCACCAGAGCCGGGAGACCCGAGCAGCCCGAGCCCGCCGAGCGCCGAGAGCGCGG -181
-180 GCGGGGGCGCGAGGCCCTGCCGCCCTTCGGTCCCCACCCCTCCGCCCTTTCCTCTCCCCACCTTCTCTCGCCTCCCGCGCCC -91
-90  CGCACCGGGCGCCCACTGTCTCTCTCTCGGGAGCGTTGTCCGTGTTGGCGGCCGACGCGGGCCGGCCGTTCCGGCGCCGGGGG -1

  1  ATGGCGCTCTGGACCTGGCCCTTGGAGGGAATGGCCGCTCTTCGGGTTTCGTCCTTCTTGGTCTGTGGCTGATGCATTTTCATGGCTATC  90
  1  M A L L D L A L E G H A V F G F V L F L V L W L M H F H A I  30

 91  ATCTACACCCGATTACACCTCAACAAGAAGGCAACTGACAAACAGCCCTTAGCAAGCTCCCAGGTGCTCTCTTCTGAAAACCACTGAAA  180
 31  I Y T R L H L N K K A T D K Q P Y S K L P G V S L L K P L K  60

181  GGGGTAGATCTTAATTAATCAACACCTGGAAACATTCTTGAATTTGGAATATCCCAAATATGAAGTGTCTCTTGTGTACAAAGATCAT  270
 61  G V D P N L I N N L E T F F E L D Y P K Y E V L L C V Q D H  90

271  GATGATCCAGCCATTGATGATGTAAGAAGCTTCTTGGAAAATATCCAAATGTTGATGCTAGATTGTTTATAGGTGGTAAAAAAGTTGGC  360
 91  D D P A I D V C K K L L G K Y P N V D A R L F I G G K K V G  120

361  ATTAATCTTAAATTAATTAATTAATGCCAGGATATGAAGTTCGAAAGTATGATCTTATATGGATTTGTGATAGTGAATAAGAGTAATT  450
121  I N P K I N N L M P G Y E V A K Y D L I W I C D S G I R V I  150

451  CCAGATACGCTTACTGACATGGTGAATCAAAATGACAGAAAAAGTAGGCTTGGTTCACGGGCTGCCTTACGTAGCAGACAGACAGGGCTTT  540
151  P T L T D M V N Q M T E K V G L V H G L P Y V A D R Q G F  180

541  GCTGCCACCTTAGAGCAGGTATAATTTGGAACATTCACATCCAAGATACTATCTCTGCCAATGTAAGTGGTTCAAATGTGTGACAGGA  630
181  A A T L E Q V Y F G T S H P R Y Y I S A H V T G F K C V T G  210

631  ATGCTTTGTTAATGAGAAAAGATGTTGGATCAAGCAGGAGGACTTATAGCTTTTGTCTCAGTACATTGCCGAAGATTACTTTATGGCC  720
211  M S C L M R K D V L D Q A G G L I A F A Q Y I A E D Y F M A  240

721  AAAGCATAGCTGACCGAGGTTGGAGGTTTGCATGTCCACTCAAGTTGCAATGCAAAACTCTGGCTCATATCAATTTCTCAGTTTCAA  810
241  K A I A D R G W R F A H S T Q V A M Q N S G S Y S I S Q F Q  270

811  TCCAGAATGATCAGGTGGACCAAACTACGAATTAACATGCTTCTCTGCTACAATAATTTGTGAGCCAAATTCAGAATGCTTTGTGCCAGT  900
271  S R M I R W T K L R I N M L P A T I I C E P I S E C F V A S  300

901  TTAATTAATGATGGGACGCCACCATGTGTTTCAGATGGATATATGGTATTTTTCATGTGTCATTCGCTGGCATGGTTTATATTTGAC  990
301  L I I G W A A H H V F R W D I H V F F M C H C L A W F I F D  330

991  TACATCAACTCAGGGGTGTCAGGGTGGCACACTGTGTTTTTCAAAAATTGATTATGACAGTGCCTGGTTCATCCGCGAATCCATGACA  1080
331  Y I Q L R G V Q G G T L C F S K L D Y A V A W F I R E S M T  360

1081  ATATACATTTTTTGTCTGCATTATGGACCCAATAAGCTGGAGAAGCTGCTGCTACAGATTACGCTGTGGGGGTACAGCAGAGGAA  1170
361  I Y I F L S A L W D P T I S W R T G R Y R L R C G G T A E E  390

1171  ATCCTAGATGATAACTACAGCTTTGACTGTATATAAAGGAAAAAAGAGAAGTATTATAAATTTATATATAAATGCTTTTAAAAA  1260
391  I L D V end  394

1261  TCTACCTTCTGTAGTTTTTATCAGATGATGTTTTGGTATCTGTCTTTAATTTATTTTTTGCATGGCCATTCGATCTGTGAAAAAAA(3') 1347
    
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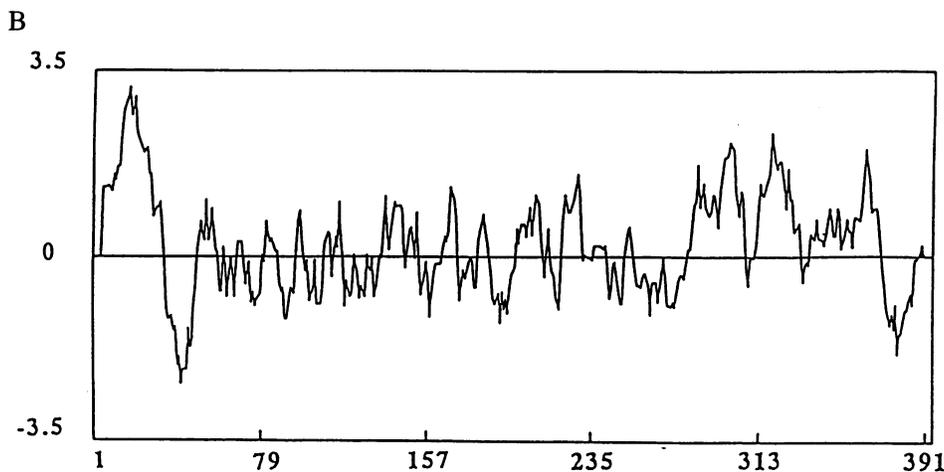


FIG. 6. (A) Nucleotide sequence and deduced amino acid sequence of GlcT-1. Putative signal-anchor sequence is underlined. (B) Hydropathy plot of the predicted amino acid sequence analyzed by the method of Kyte and Doolittle with a window of 10 (31). Positive values represent increased hydrophobicity.